


```

QY 1 MRAKATGTHNAGKALAGAAAGAAKATCAAAWAVAAAMALVAAVAVAAWAAVAAV 60
DB 1 MRAKATGTHNAGKALAGAAAGAAKATCAAAWAVAAAMALVAAVAVAAWAAVAAV 60
QY 1 MRAKATGTHNAGKALAGAAAGAAKATCAAAWAVAAAMALVAAVAVAAWAAVAAV 60
DB 1 MRAKATGTHNAGKALAGAAAGAAKATCAAAWAVAAAMALVAAVAVAAWAAVAAV 60
QY 61 AASSLRLQNSPTLRLAERATVAAVTHVYVAVVTHVYVAVVTHVYVAVVTHVYV 120
DB 61 AASSLRLQNSPTLRLAERATVAAVTHVYVAVVTHVYVAVVTHVYVAVVTHVYV 120
QY 121 SAPNVLVATGTHNAGKALAGAAAGAAKATCAAAWAVAAAMALVAAVAVAAWAAV 180
DB 121 SAPNVLVATGTHNAGKALAGAAAGAAKATCAAAWAVAAAMALVAAVAVAAWAAV 180
QY 181 SSIPPEHVAERPEVTHVYVAVVTHVYVAVVTHVYVAVVTHVYVAVVTHVYV 240
DB 181 SSIPPEHVAERPEVTHVYVAVVTHVYVAVVTHVYVAVVTHVYVAVVTHVYV 240
QY 241 GPEPTPEAGSPSPPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPT 300
DB 241 GPEPTPEAGSPSPPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPT 300
QY 301 ASPTSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS 360
DB 301 ASPTSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS 360
QY 361 AVTVSSTPEHVAERPEVTHVYVAVVTHVYVAVVTHVYVAVVTHVYVAVVTHVYV 420
DB 361 AVTVSSTPEHVAERPEVTHVYVAVVTHVYVAVVTHVYVAVVTHVYVAVVTHVYV 420
QY 421 RAVTPEHVAERPEVTHVYVAVVTHVYVAVVTHVYVAVVTHVYVAVVTHVYV 445
DB 421 RAVTPEHVAERPEVTHVYVAVVTHVYVAVVTHVYVAVVTHVYVAVVTHVYV 445

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RESULT 6

AA060627 Standard: Protein: 445 AA.

AC AAB0627;

XX 19-MAR-2001 (first entry)

DE A human histamine H4 receptor polypeptide.

EW Human: histamine H4 receptor; inflammation; allergy.

XX Homo sapiens.

IN OS616559-A.

XX 24-SEP-2000.

XX 07-07-1996. 5005-016764.

XX 07-07-1996. 9605-016764.

XX (ORION) ORION PHARM CORP.

XX Lovrenberg TW, Pyati J, Erlanker M, Buzari A.

XX WPL 2001-023168/01.

XX N-TSDB: AA062466.

XX Novel DNA molecules useful in gene therapy for the treatment of

XX inflammation or allergy, or for encoding a human histamine H4 receptor

XX and identifying histamine receptor modulators that are useful as

XX therapeutic and diagnostic agents

XX Example 4: Fig 4; 2pp; English.

XX The present sequence represents human histamine H4 receptor, the

XX histamine H4 receptor DNA molecules are useful for isolating

XX homologues of receptor, identifying and isolating genomic equivalents

of receptor, and identifying, detecting or isolating mutant forms of the receptor. The DNA molecules are also useful in gene therapy for the treatment of inflammation or allergy. The human histamine H4 receptor protein is useful in identifying modulators of the human histamine H4 receptor, which in turn are useful as therapeutic and diagnostic agents.

XX Sequence 445 AA.

QY Query Match: 98.18; Score: 2457; ID: 22; Length: 445;

DB Local: 55.08; First: No; 7 sec: 184;

Matches: 444; Conservative: 1; Mismatches: 0; Models: 0; Gaps: 0;

QY 1 MRAKATGTHNAGKALAGAAAGAAKATCAAAWAVAAAMALVAAVAVAAWAAVAAV 60

DB 1 MRAKATGTHNAGKALAGAAAGAAKATCAAAWAVAAAMALVAAVAVAAWAAVAAV 60

QY 61 AASSLRLQNSPTLRLAERATVAAVTHVYVAVVTHVYVAVVTHVYVAVVTHVYV 120

DB 61 AASSLRLQNSPTLRLAERATVAAVTHVYVAVVTHVYVAVVTHVYVAVVTHVYV 120

QY 121 SAPNVLVATGTHNAGKALAGAAAGAAKATCAAAWAVAAAMALVAAVAVAAWAAV 180

DB 121 SAPNVLVATGTHNAGKALAGAAAGAAKATCAAAWAVAAAMALVAAVAVAAWAAV 180

QY 181 SSIPPEHVAERPEVTHVYVAVVTHVYVAVVTHVYVAVVTHVYVAVVTHVYV 240

DB 181 SSIPPEHVAERPEVTHVYVAVVTHVYVAVVTHVYVAVVTHVYVAVVTHVYV 240

QY 241 GPEPTPEAGSPSPPT 300

DB 241 GPEPTPEAGSPSPPT 300

QY 301 ASPTSS 360

DB 301 ASPTSS 360

QY 361 AVTVSSTPEHVAERPEVTHVYVAVVTHVYVAVVTHVYVAVVTHVYVAVVTHVYV 420

DB 361 AVTVSSTPEHVAERPEVTHVYVAVVTHVYVAVVTHVYVAVVTHVYVAVVTHVYV 420

QY 421 RAVTPEHVAERPEVTHVYVAVVTHVYVAVVTHVYVAVVTHVYVAVVTHVYV 445

DB 421 RAVTPEHVAERPEVTHVYVAVVTHVYVAVVTHVYVAVVTHVYVAVVTHVYV 445

RESULT 7

AA060623

DE AA060623 Standard: Protein: 445 AA.

XX AC AAY06023;

XX 06-SEP-1999 (first entry)

DE Rat G protein coupled receptor r1b4q5.

XX G protein coupled receptor: r1b4q5; rat; diagnosis; screening;

XX therapy; anti-kinsonia; neuroprotection; neuroprotective;

XX neurolytic; and antidepressant; and anti-epilepsy; and idiopathic;

XX anti-inflammatory; phosphatidylinositol.

XX Rattus sp.

XX Key: local/only/qualifiers

FI domain 40..59 "transmembrane domain"

FI domain 74..91 "transmembrane domain"

FI domain 109..140 "transmembrane domain"

FI domain 152..174 "transmembrane domain"

FI domain 175..191 "transmembrane domain"


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Query Match      76.1%  Score 1828;  DB 20;  Length 462;
Best Local Similarity 92.8%;  Pred. No. 6,96 141;
Matches 347;  Conserved 8;  Mismatches 16;  Indels 2;  Gaps 2;

QY 84 GAFCLPYAVPVLCGRWTFQRGAKLAVAVYLDLTSSAFKLVLLDGRKLVAVKAVYK 143
DB 1 GATCLPYAVPVLCGRWTFQRGAKLAVAVYLDLTSSAFKLVLLDGRKLVAVKAVYK 60

QY 144 AQGCHTRAVAKMLLVWVLAFLTGPAHLSWETLSQSSATLGGHCVATVYVRYPLTAS 203
DB 61 AQGCHTRAVAKMLLVWVLAFLTGPAHLSWETLSQSSATLGGHCVATVYVRYPLTAS 120

QY 204 TLEFFTPPLSVTFENISYINIGRKIRGRLGAKAWARLILZGLZGL 262
DB 121 TLEFFTPPLSVTFENISYINIGRKIRGRLGAKAWARLILZGLZGL 179

QY 263 QNGCHTRAVAKMLLVWVLAFLTGPAHLSWETLSQSSATLGGHCVATVYVRYPLTAS 322
DB 180 QNGCHTRAVAKMLLVWVLAFLTGPAHLSWETLSQSSATLGGHCVATVYVRYPLTAS 239

QY 323 QNGCHTRAVAKMLLVWVLAFLTGPAHLSWETLSQSSATLGGHCVATVYVRYPLTAS 382
DB 240 QNGCHTRAVAKMLLVWVLAFLTGPAHLSWETLSQSSATLGGHCVATVYVRYPLTAS 299

QY 483 AQGCHTRAVAKMLLVWVLAFLTGPAHLSWETLSQSSATLGGHCVATVYVRYPLTAS 442
DB 300 AQGCHTRAVAKMLLVWVLAFLTGPAHLSWETLSQSSATLGGHCVATVYVRYPLTAS 400

QY 443 GAK 445
DB 460 GAK 462

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RESULT 13
AAW92977
ID AAW92977 standard; Protein: 470 AA.
XX AAW92977;
DE P1: mAHR 6, protein fragment
XX mAHR-6; muscarinic acetylcholine receptor 6; disorder; secretion;
XX acetylcholine responsive cells; phosphatidylinositol turn-over;
XX smooth muscle cell contraction; nervous system disorder; glandular;
XX Schizoaffective disorder; affective disorder; sleep disorder;
XX megalencephalic disorder; eating disorder; drinking disorder; rat.
XX Rattus sp.
XX Key Location/Qualifiers
XX Protein 1-470
XX Gene Muscarinic acetylcholine receptor 6, rat
XX Gene Muscarinic acetylcholine receptor 6, rat
XX 16 MAP 1999
XX 04 DBJ 1997; 9705-0985090.
XX 04 DBJ 1997; 9705-0985090.
XX (MILL-) MLLTRR30X PHAGE INC.
XX Goodcart AB;
XX WPI; 1999-214063/18.
XX N-PSDB; AAW92889.
XX Nucleic acids encoding muscarinic acetylcholine receptor 6 - useful
XX for modulating the effects of acetylcholine on acetylcholine
XX responsive cells
XX

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XX this invention describes the isolation of a novel human muscarinic
XX acetylcholine receptor 6 (mAHR 6), capable of modulating the effects
XX of acetylcholine on acetylcholine responsive cells. mAHR 6 cDNA and
XX polypeptides may be used to detect naturally occurring mutations of the
XX mAHR 6 gene and determine if a subject with the mutated gene is at risk
XX of (or is predisposed to have) a mAHR 6 related disorder, mediated by
XX activity mediated by mAHR 6 (e.g., behavioral processes mediated by
XX phosphatidylinositol turn-over and signaling), secretion of a mediator
XX (e.g., a neurotransmitter or a glandular enzyme), or contraction of a
XX smooth muscle cell, treat disorders mediated by abnormal mAHR 6 activity
XX e.g. nervous system disorders (e.g., amnesia, ataxia, anorexia,
XX dystonia), amnesia spatial disorientation, Kliver-Bucy syndrome,
XX Alzheimer's related memory loss and learning disability, visual
XX hallucinations, perceptual disturbances, and Lewy body dementia
XX associated delirium, schizophrenia disorders (e.g. schizophrenia
XX with mood swings, and depressive illness), paroxysmal sleep abnormality
XX disorders (e.g. REM sleep abnormalities), paroxysmal sleep depression
XX sleep-wakefulness, and body temperature or respiratory depression
XX abnormalities during sleep), pain denervation mechanism disorders (e.g.
XX related to irritable bowel syndrome (IBS), or chest pain), movement
XX disorders (e.g. related to Parkinson's disease), eating disorders (e.g.
XX insulin hypersecretion related obesity), drinking disorders (e.g.
XX diabetic polydipsia), smooth muscle related disorders (e.g. IBS,
XX diverticular disease), urinary incontinence, oesophageal achalasia, and
XX chronic obstructive airways disease, cardiac disorders (e.g. pathological
XX bradycardia or tachycardia, arrhythmia, flutter and fibrillation), and
XX glandular disorders (e.g. xerostomia and diabetes mellitus).
XX
XX Sequence 470 AA:

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Query Match      76.1%  Score 1828;  DB 20;  Length 470;
Best Local Similarity 92.8%;  Pred. No. 7,16 141;
Matches 347;  Conserved 8;  Mismatches 16;  Indels 2;  Gaps 2;

QY 64 GAFCLPYAVPVLCGRWTFQRGAKLAVAVYLDLTSSAFKLVLLDGRKLVAVKAVYK 143
DB 9 GATCLPYAVPVLCGRWTFQRGAKLAVAVYLDLTSSAFKLVLLDGRKLVAVKAVYK 60

QY 144 AQGCHTRAVAKMLLVWVLAFLTGPAHLSWETLSQSSATLGGHCVATVYVRYPLTAS 203
DB 61 AQGCHTRAVAKMLLVWVLAFLTGPAHLSWETLSQSSATLGGHCVATVYVRYPLTAS 120

QY 204 TLEFFTPPLSVTFENISYINIGRKIRGRLGAKAWARLILZGLZGL 262
DB 121 TLEFFTPPLSVTFENISYINIGRKIRGRLGAKAWARLILZGLZGL 179

QY 263 QNGCHTRAVAKMLLVWVLAFLTGPAHLSWETLSQSSATLGGHCVATVYVRYPLTAS 322
DB 180 QNGCHTRAVAKMLLVWVLAFLTGPAHLSWETLSQSSATLGGHCVATVYVRYPLTAS 239

QY 323 QNGCHTRAVAKMLLVWVLAFLTGPAHLSWETLSQSSATLGGHCVATVYVRYPLTAS 382
DB 240 QNGCHTRAVAKMLLVWVLAFLTGPAHLSWETLSQSSATLGGHCVATVYVRYPLTAS 299

QY 483 AQGCHTRAVAKMLLVWVLAFLTGPAHLSWETLSQSSATLGGHCVATVYVRYPLTAS 442
DB 300 AQGCHTRAVAKMLLVWVLAFLTGPAHLSWETLSQSSATLGGHCVATVYVRYPLTAS 400

QY 443 GAK 445
DB 460 GAK 462

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RESULT 14
AAW71297
ID AAW71297 standard; Protein: 490 AA.
XX AAW71297;
XX

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Thu Jan 10 14:46:49 2002

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PR 40 JUN-1999; 99US-0141448.
PR 27-AUG-1999; 99US-0151114.
PR 03-SEP-1999; 99US-0152524.
PR 29-SEP-1999; 99US-0156633.
PR 29-SEP-1999; 99US-0156655.
PR 29-SEP-1999; 99US-0156664.
XX
XX (AKER) 3 AKERA PHARM 180.
XX
XX Behan DP, Lehmann-Bruinsma K, Chalmers DL, Chen K, Dant HL;
XX Gore M, Liao CW, Lin L, Lowitt K, White C;
XX WPI; 2000-07-06/27.
XX N-15DB; AAA46023.
XX
XX Non-endogenous, human G protein-coupled receptors for screening
XX receptor, inverse or partial agonists useful as therapeutic agents
XX
XX Example 1; Page 89-90; 187pp; English.
XX
XX The present invention describes transmembrane receptors, preferably
XX human G protein coupled receptors (GPCR), for which the endogenous
XX ligand is unknown (orphan GPCR receptors). More specifically the present
XX invention relates to non-endogenous, constitutively activated versions
XX of a human GPCR. These non-endogenous human GPCRs can be useful for
XX the direct identification of candidate compounds as receptors agonists,
XX inverse agonists or partial agonists for use as pharmaceutical agents.
XX AAA46017 to AAA46126 and AAA02825 to AAA02859 represent sequences used in
XX the exemplification of the present invention.
XX
XX Sequence 490 AA;
XX
Query Match 40.1%; Score 724; DB 21; Length 490;
Best Local Similarity 48.6%; Prod. No. 5; Lc 51;
Matches 164; Conservative 56; Mismatches 131; Indels 74; Gaps 10;
QY 40 SAARTAVLAALMALIVAVLGNALVMAAFVASSLRFGNRIETLLNLAIISFLVGAFCIP 89
Db 11 SLSRLVLAIRMAIVLALFALFALFALFALFALFALFALFALFALFALFALFALF 70
QY 90 LAYIVVLAIVKIVKRGCKLWAVVYVLLTSSAPNIVLISYDPPISVDAVASVRAQKQDF 149
Db 11 L1111111111111111111111111111111111111111111111111111111 120
QY 71 LYPHLLQWDFKLVGLVGLVGLVGLVGLVGLVGLVGLVGLVGLVGLVGLVGLVGLV 120
Db 11 L1111111111111111111111111111111111111111111111111111111 181
QY 150 RAVRAMLVWVLAFLVGLVGLVGLVGLVGLVGLVGLVGLVGLVGLVGLVGLVGLVGL 205
Db 11 L1111111111111111111111111111111111111111111111111111111 181
QY 140 LKLVLAAGVGLVGLVGLVGLVGLVGLVGLVGLVGLVGLVGLVGLVGLVGLVGLV 205
Db 11 L1111111111111111111111111111111111111111111111111111111 265
QY 206 EPTDFLSVTFNLSIYLNLFQRTKRLDGAKIAAGHETPPDAQSPDPDPGQWQWQK 265
Db 11 L1111111111111111111111111111111111111111111111111111111 205
QY 182 GIVPPIVAYTNNLY-----WSLWKID 205
QY 266 DGEAMPLIRYGVGAAVAGACAGATLRRGGGGGVASPTSSSGSS-----SRPTFRPR 318
Db 206 HLRGQSH-----PALLVSSNLSQSHSHPQRTSSRSLSASTQVPASTHSGRTKRS 257
QY 319 GLKGGGRTFAASAEPTPEWVAGAPW-----CPPIQDPVPFVAKSLAVINSIFPLWA 472
Db 11 L1111111111111111111111111111111111111111111111111111111 317
QY 258 SLMSISRTKMSIHLASKJSTSLSDSLVATHQCHVLLRRRLAKSLALIAVAVCW 417
QY 473 PYLLMLTRACALHCKVPLWYETFSWELAKASAVNIVLYPLQHSFEPAPFRLTPQAK 431
Db 418 PYSLLTVLSLYSSATQPKSOWYRIALWQWHTSTVQPLTFYCHKRTPKATLKLTP 474
QY 432 LKIQD 436
Db 475 LKKIP 479

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[illegible][illegible]


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QY 429 F SAGELEMPVGLGCGSGSGLGSSVAVDCAVALVELLALHLLKADMLRGG 429
Db 240 SHMIFEPFPGV          IIIIIIII  I  I  I  I  I  I  I  I  I  I
QY 438 NTEGVNLSRLMALAGVAVLVNLSRHDEATPTTSTPFLPLDVLINCKWTFM 447
Db 289 QNVIVLKHLYCNYLVNIVSLTNMTETETETELLE             IIII
QY 449 F 449
Db 454 E 454

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RESULT 15
 PCT-USA: 387528-13
 ? Sequence 13, Application PC/TUS9008528
 ? GENERAL INFORMATION:
 ? APPLICANT: New York University
 ? TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
 ? TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
 ? NUMBER OF SEQUENCES: 348
 ? CORRESPONDENCE ADDRESS:
 ? ADDRESSEE: BOWEN AND STRIMARK
 ? STREET: 419 Seventh Street, N.W., Suite 300
 ? CITY: Washington
 ? STATE: D.C.
 ? COUNTRY: USA
 ? ZIP: 20004
 ? COMPUTER READABLE FORM:
 ? MEDIUM TYPE: Floppy disk
 ? COMPUTER: IBM PC compatible
 ? OPERATING SYSTEM: PC-DOS/MS-DOS
 ? SOFTWARE: Patent In Release #1.0, Version #1.25
 ? CURRENT APPLICATION DATA:
 ? APPLICATION NUMBER: PC/TUS9108528
 ? FILING DATE: 09-SEP-1993
 ? PRIOR APPLICATION DATA:
 ? APPLICATION NUMBER: US 07/944,246
 ? FILING DATE: 10-SEP-1992
 ? ATTORNEY/AGENT INFORMATION:
 ? NAME: Townsend, Kevin G.
 ? REGISTRATION NUMBER: 34,033
 ? REFERENCE/CHECK NUMBER: MURPHY 2 PCT
 ? TELECOMMUNICATION INFORMATION:
 ? TELEPHONE: 202-628-5197
 ? TELEFAX: 202-747-4528
 ? TELEX: 248633
 ? INFORMATION FOR SEQ ID NO: 13:
 ? SEQUENCE CHARACTERISTICS:
 ? LENGTH: 348 amino acids
 ? TYPE: amino acid
 ? STRANDEDNESS: single
 ? TOPOLOGY: linear
 ? MOLECULE TYPE: peptide
 ? PCT-ISA: 387528-13

[illegible]


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1021 TGGCAAGCTTCACGAGAGGATTTGAGAGTGTGAGAGAGCAAGTGGTAAAGTACAGCTG 1080
1351 aagcctcatcatgaatctcttgaqctctgaqctctgaqctctgaqctctgaqctctgaqctct 1410
1081 GAGGTCATGCTGACGATCTTGGGCTCTGTGTGCTGGGCTATACACGCTGTGGAGAGATATG 1140
1411 ctatgaatctgaatctctgaqctctgaqctctgaqctctgaqctctgaqctctgaqctct 1470
1141 GAGGTCATGCTGACGATCTTGGGCTCTGTGTGCTGGGCTATACACGCTGTGGAGAGATATG 1200
1471 ctatgaatctgaatctctgaqctctgaqctctgaqctctgaqctctgaqctctgaqctct 1530
1201 CTGTGGGCTCAACCTGGGCTGTGAACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1260
1541 ctatgaatctgaatctctgaqctctgaqctctgaqctctgaqctctgaqctctgaqctct 1599
1261 GAGGCTCTGCAAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1320
1591 aagcctcatcatgaatctcttgaqctctgaqctctgaqctctgaqctctgaqctctgaqctct 1642
1421 GAACTATGCTGAGAAAGATGAAGAAGAAAGAAATGCTGTGTGA 1462

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RESULT 4
AK104201
LOCUS AR104201 2689 bp DNA PAT 14 FEB 2001
DEFINITION Sequence from patent US 6,093,455.
ACCESSION AR104201
VERSION AR104201.1 31-12-1999
KEYWORDS unknown.
SOURCE unknown.
ORGANISM unknown.
REFERENCE 1 (bases 1 to 2689)
AUTHORS Goodbar, A. D. J. and Glycksmann, M. Alexandra.
TITLE Methods for detecting nucleic acid molecules encoding a member of the muscarinic family of receptors
JOURNAL patent: US 6,093,455-A 1 25-JUL-2000
FEATURES *locus_tag* = *gagaa*; *locus_id* = 1; *length* = 2689
SOURCE *organism* = "unknown"
BASE COUNT 993 a 990 c 806 g 500 t
ORIGIN

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Query Match 66.48% Score 1360.4; DB 6; Length 2689;
Best Local Similarity 99.94%; Init'd. Max. 188;
Matches 1461; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 243 TGGCAAGCTTCACGAGAGGATTTGAGAGTGTGAGAGAGCAAGTGGTAAAGTACAGCTG 402
DB 263 TGGCAAGCTTCACGAGAGGATTTGAGAGTGTGAGAGAGCAAGTGGTAAAGTACAGCTG 422
QY 403 TGGCAAGCTTCACGAGAGGATTTGAGAGTGTGAGAGAGCAAGTGGTAAAGTACAGCTG 462
DB 423 TGGCAAGCTTCACGAGAGGATTTGAGAGTGTGAGAGAGCAAGTGGTAAAGTACAGCTG 482
QY 463 TGGCAAGCTTCACGAGAGGATTTGAGAGTGTGAGAGAGCAAGTGGTAAAGTACAGCTG 422
DB 483 TGGCAAGCTTCACGAGAGGATTTGAGAGTGTGAGAGAGCAAGTGGTAAAGTACAGCTG 442
QY 443 TGGCAAGCTTCACGAGAGGATTTGAGAGTGTGAGAGAGCAAGTGGTAAAGTACAGCTG 482
DB 443 TGGCAAGCTTCACGAGAGGATTTGAGAGTGTGAGAGAGCAAGTGGTAAAGTACAGCTG 502
QY 483 TGGCAAGCTTCACGAGAGGATTTGAGAGTGTGAGAGAGCAAGTGGTAAAGTACAGCTG 542
DB 503 TGGCAAGCTTCACGAGAGGATTTGAGAGTGTGAGAGAGCAAGTGGTAAAGTACAGCTG 562
QY 543 TGGCAAGCTTCACGAGAGGATTTGAGAGTGTGAGAGAGCAAGTGGTAAAGTACAGCTG 602
DB 563 TGGCAAGCTTCACGAGAGGATTTGAGAGTGTGAGAGAGCAAGTGGTAAAGTACAGCTG 622

QY 603 TGGCAAGCTTCACGAGAGGATTTGAGAGTGTGAGAGAGCAAGTGGTAAAGTACAGCTG 662
DB 623 TGGCAAGCTTCACGAGAGGATTTGAGAGTGTGAGAGAGCAAGTGGTAAAGTACAGCTG 682
QY 663 TGGCAAGCTTCACGAGAGGATTTGAGAGTGTGAGAGAGCAAGTGGTAAAGTACAGCTG 722
DB 683 TGGCAAGCTTCACGAGAGGATTTGAGAGTGTGAGAGAGCAAGTGGTAAAGTACAGCTG 742
QY 723 TGGCAAGCTTCACGAGAGGATTTGAGAGTGTGAGAGAGCAAGTGGTAAAGTACAGCTG 782
DB 743 TGGCAAGCTTCACGAGAGGATTTGAGAGTGTGAGAGAGCAAGTGGTAAAGTACAGCTG 802
QY 783 TGGCAAGCTTCACGAGAGGATTTGAGAGTGTGAGAGAGCAAGTGGTAAAGTACAGCTG 842
DB 803 TGGCAAGCTTCACGAGAGGATTTGAGAGTGTGAGAGAGCAAGTGGTAAAGTACAGCTG 862
QY 843 TGGCAAGCTTCACGAGAGGATTTGAGAGTGTGAGAGAGCAAGTGGTAAAGTACAGCTG 902
DB 863 TGGCAAGCTTCACGAGAGGATTTGAGAGTGTGAGAGAGCAAGTGGTAAAGTACAGCTG 922
QY 903 TGGCAAGCTTCACGAGAGGATTTGAGAGTGTGAGAGAGCAAGTGGTAAAGTACAGCTG 962
DB 923 TGGCAAGCTTCACGAGAGGATTTGAGAGTGTGAGAGAGCAAGTGGTAAAGTACAGCTG 982
QY 963 TGGCAAGCTTCACGAGAGGATTTGAGAGTGTGAGAGAGCAAGTGGTAAAGTACAGCTG 1022
DB 983 TGGCAAGCTTCACGAGAGGATTTGAGAGTGTGAGAGAGCAAGTGGTAAAGTACAGCTG 1042
QY 1023 TGGCAAGCTTCACGAGAGGATTTGAGAGTGTGAGAGAGCAAGTGGTAAAGTACAGCTG 1082
DB 1043 TGGCAAGCTTCACGAGAGGATTTGAGAGTGTGAGAGAGCAAGTGGTAAAGTACAGCTG 1102
QY 1083 TGGCAAGCTTCACGAGAGGATTTGAGAGTGTGAGAGAGCAAGTGGTAAAGTACAGCTG 1142
DB 1103 TGGCAAGCTTCACGAGAGGATTTGAGAGTGTGAGAGAGCAAGTGGTAAAGTACAGCTG 1162
QY 1143 TGGCAAGCTTCACGAGAGGATTTGAGAGTGTGAGAGAGCAAGTGGTAAAGTACAGCTG 1202
DB 1163 TGGCAAGCTTCACGAGAGGATTTGAGAGTGTGAGAGAGCAAGTGGTAAAGTACAGCTG 1222
QY 1203 TGGCAAGCTTCACGAGAGGATTTGAGAGTGTGAGAGAGCAAGTGGTAAAGTACAGCTG 1262
DB 1223 TGGCAAGCTTCACGAGAGGATTTGAGAGTGTGAGAGAGCAAGTGGTAAAGTACAGCTG 1282
QY 1263 TGGCAAGCTTCACGAGAGGATTTGAGAGTGTGAGAGAGCAAGTGGTAAAGTACAGCTG 1342
DB 1283 TGGCAAGCTTCACGAGAGGATTTGAGAGTGTGAGAGAGCAAGTGGTAAAGTACAGCTG 1362
QY 1343 TGGCAAGCTTCACGAGAGGATTTGAGAGTGTGAGAGAGCAAGTGGTAAAGTACAGCTG 1382
DB 1363 TGGCAAGCTTCACGAGAGGATTTGAGAGTGTGAGAGAGCAAGTGGTAAAGTACAGCTG 1402
QY 1383 TGGCAAGCTTCACGAGAGGATTTGAGAGTGTGAGAGAGCAAGTGGTAAAGTACAGCTG 1442
DB 1403 TGGCAAGCTTCACGAGAGGATTTGAGAGTGTGAGAGAGCAAGTGGTAAAGTACAGCTG 1462
QY 1443 TGGCAAGCTTCACGAGAGGATTTGAGAGTGTGAGAGAGCAAGTGGTAAAGTACAGCTG 1502
DB 1463 TGGCAAGCTTCACGAGAGGATTTGAGAGTGTGAGAGAGCAAGTGGTAAAGTACAGCTG 1522
QY 1503 TGGCAAGCTTCACGAGAGGATTTGAGAGTGTGAGAGAGCAAGTGGTAAAGTACAGCTG 1562
DB 1523 TGGCAAGCTTCACGAGAGGATTTGAGAGTGTGAGAGAGCAAGTGGTAAAGTACAGCTG 1582
QY 1563 TGGCAAGCTTCACGAGAGGATTTGAGAGTGTGAGAGAGCAAGTGGTAAAGTACAGCTG 1602
DB 1583 TGGCAAGCTTCACGAGAGGATTTGAGAGTGTGAGAGAGCAAGTGGTAAAGTACAGCTG 1622

RESULT 4
AK104201
LOCUS AR104201 2689 bp DNA PAT 14 FEB 2001

```

DEFINITION Sequence 5 from patient US 6136559.
ACCESSION AK13732
VERSION AK13732.1 GI:114476404
KEYWORDS
SOURCE Unknown.
ORGANISM Hominidae.
REFERENCE 1 (bases 1 to 2699)
AUTHORS Loveland J.W., Kollander M., Hovatt A. and Pyatt J.
TITLE RNA encoding as human histamine receptor of the H4 subtype
JOURNAL Patient US 6136559-A 6 24 2001-2002
FEATURES
location/Qualifiers
1..2699
BASE COUNT 404 A 988 C 805 G 502 T
ORIGIN
1
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	Best Match	Similarity	Conservative	Q	Mismatches	Indels	6	Gaps	2
QY	243	500	99.99	100	0	0	0	0	0
DB	1487	500	99.99	100	0	0	0	0	0
QY	405	500	99.99	100	0	0	0	0	0
DB	470	500	99.99	100	0	0	0	0	0
QY	463	500	99.99	100	0	0	0	0	0
DB	430	500	99.99	100	0	0	0	0	0
QY	423	500	99.99	100	0	0	0	0	0
DB	490	500	99.99	100	0	0	0	0	0
QY	483	500	99.99	100	0	0	0	0	0
DB	550	500	99.99	100	0	0	0	0	0
QY	543	500	99.99	100	0	0	0	0	0
DB	610	500	99.99	100	0	0	0	0	0
QY	603	500	99.99	100	0	0	0	0	0
DB	670	500	99.99	100	0	0	0	0	0
QY	663	500	99.99	100	0	0	0	0	0
DB	730	500	99.99	100	0	0	0	0	0
QY	723	500	99.99	100	0	0	0	0	0
DB	790	500	99.99	100	0	0	0	0	0
QY	843	500	99.99	100	0	0	0	0	0
DB	910	500	99.99	100	0	0	0	0	0
QY	903	500	99.99	100	0	0	0	0	0
DB	970	500	99.99	100	0	0	0	0	0
QY	963	500	99.99	100	0	0	0	0	0
DB	1040	500	99.99	100	0	0	0	0	0
QY	1023	500	99.99	100	0	0	0	0	0
DB	1087	500	99.99	100	0	0	0	0	0
QY	1080	500	99.99	100	0	0	0	0	0
DB	1147	500	99.99	100	0	0	0	0	0
QY	1140	500	99.99	100	0	0	0	0	0
DB	1207	500	99.99	100	0	0	0	0	0
QY	1200	500	99.99	100	0	0	0	0	0
DB	1267	500	99.99	100	0	0	0	0	0
QY	1260	500	99.99	100	0	0	0	0	0

DB	1427	500	99.99	100	0	0	0	0	0
QY	1430	500	99.99	100	0	0	0	0	0
DB	1487	500	99.99	100	0	0	0	0	0
QY	1480	500	99.99	100	0	0	0	0	0
DB	1447	500	99.99	100	0	0	0	0	0
QY	1440	500	99.99	100	0	0	0	0	0
DB	1507	500	99.99	100	0	0	0	0	0
QY	1500	500	99.99	100	0	0	0	0	0
DB	1567	500	99.99	100	0	0	0	0	0
QY	1560	500	99.99	100	0	0	0	0	0
DB	1627	500	99.99	100	0	0	0	0	0
RESULT	9								
DEFINITION	Sequence 4, 1100, patient US 6093545.								
ACCESSION	AF004203								
VERSION	AF004203.1								
KEYWORDS	Sequence, 1100, patient US 6093545.								
FEATURES	Location/Qualifiers								
BASE COUNT	609 a 1052 c 963 g 680 t								
ORIGIN									
Query Match	53.38%	Score 1094	DB 6	Length 3244					
Best Local Similarity	88.6%	Prod. No. 1.5e-119							
Matches 1209	Conservative	0	Mismatches 150	Indels 6	Gaps 2				
QY	243	500	99.99	100	0	0	0	0	0
DB	750	500	99.99	100	0	0	0	0	0
QY	603	500	99.99	100	0	0	0	0	0
DB	810	500	99.99	100	0	0	0	0	0
QY	963	500	99.99	100	0	0	0	0	0
DB	870	500	99.99	100	0	0	0	0	0
QY	423	500	99.99	100	0	0	0	0	0
DB	940	500	99.99	100	0	0	0	0	0
QY	405	500	99.99	100	0	0	0	0	0
DB	960	500	99.99	100	0	0	0	0	0
QY	543	500	99.99	100	0	0	0	0	0
DB	1050	500	99.99	100	0	0	0	0	0

AUTHORS: Gordon, L.A., D.J., and Glicksman, R., Alexandria.
 TITLE: Methods for detecting nucleic acid molecules encoding a member of
 the muscarinic family of receptors.
 JOURNAL: Patent: US 6093545-A 4 21, 001, 2000.
 FEATURES: Location/Qualifiers
 1..3244
 609 a 1052 c 963 g 680 t

GeneTools version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
us-09-891-053-20.rspt
Protein - protein search, using sw model
Run on: January 10, 2002, 14:41:15 ; Search time 56.45 Seconds
(without alignment)
1173,806 Million cell updates/sec
Title: us-09-891-053-20
Perfect score: 2403
Sequence: 1 MERAP10CTHNA5ALALAEA.....IGHHSLEHPWETPEKKEK 453

Search table: BLAST06.2
Gapop 10.0 ; Gapext 0.5
Searched: 473505 seqs, 14527329 residues
Total number of hits satisfying chosen parameters: 473505
Minimum db seq length: 0
Maximum db seq length: 200000000
Post-processing: Minimum Match: 40
Maximum Match: 100%
Listing first 4% summaries

Database: SPTRMBL_173*
1: SP archaea*
2: SP bacteria*
3: SP fungi*
4: SP human*
5: SP invertebrates*
6: SP mammal*
7: SP mhc*
8: SP organelle*
9: SP phage*
10: SP plant*
11: SP rodent*
12: SP virus*
13: SP vertebrate*
14: SP unclassified*
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	IP	ID	Accession
1	2403	100.0	453	4	Q962X2	Q962X2 homo sapien
2	2360	98.2	415	4	Q962X2	Q962X2 homo sapien
3	2357	98.1	445	4	Q962X1	Q962X1 homo sapien
4	2315	94.2	445	11	Q962X9	Q962X9 ratius norv
5	2182	90.8	415	11	Q962X6	Q962X6 ratius norv
6	2060	85.7	413	11	Q962X7	Q962X7 ratius norv
7	2045	85.1	415	11	Q962X5	Q962X5 cavia porce
8	1975	82.2	497	11	Q962X6	Q962X6 ratius norv
9	1685	70.1	445	11	Q962X9	Q962X9 ratius norv
10	553.5	23.0	528	13	Q962X6	Q962X6 ratius norv
11	511	21.3	440	4	Q962X9	Q962X9 homo sapien
12	511	21.3	440	6	Q962X7	Q962X7 par. A. n. n. l.
13	511	21.3	440	6	Q962X6	Q962X6 quilla qor
14	509	21.2	440	6	Q962X6	Q962X6 poapo pyama
15	506	21.1	399	5	Q962X9	Q962X9 apis mellif
16	492	20.5	462	4	Q962X9	Q962X9 homo sapien
17	489.5	20.4	450	4	Q962X1	Q962X1 homo sapien
18	474.5	19.7	447	4	Q962X0	Q962X0 homo sapien
19	458.5	19.1	477	5	Q962X9	Q962X9 mus muscu

SUMMARIES

Result No.	Score	Query Match	Length	IP	ID	Accession
1	2403	100.0	453	4	Q962X2	Q962X2 homo sapien
2	2360	98.2	415	4	Q962X2	Q962X2 homo sapien
3	2357	98.1	445	4	Q962X1	Q962X1 homo sapien
4	2315	94.2	445	11	Q962X9	Q962X9 ratius norv
5	2182	90.8	415	11	Q962X6	Q962X6 ratius norv
6	2060	85.7	413	11	Q962X7	Q962X7 ratius norv
7	2045	85.1	415	11	Q962X5	Q962X5 cavia porce
8	1975	82.2	497	11	Q962X6	Q962X6 ratius norv
9	1685	70.1	445	11	Q962X9	Q962X9 ratius norv
10	553.5	23.0	528	13	Q962X6	Q962X6 ratius norv
11	511	21.3	440	4	Q962X9	Q962X9 homo sapien
12	511	21.3	440	6	Q962X7	Q962X7 par. A. n. n. l.
13	511	21.3	440	6	Q962X6	Q962X6 quilla qor
14	509	21.2	440	6	Q962X6	Q962X6 poapo pyama
15	506	21.1	399	5	Q962X9	Q962X9 apis mellif
16	492	20.5	462	4	Q962X9	Q962X9 homo sapien
17	489.5	20.4	450	4	Q962X1	Q962X1 homo sapien
18	474.5	19.7	447	4	Q962X0	Q962X0 homo sapien
19	458.5	19.1	477	5	Q962X9	Q962X9 mus muscu

Query Match: 100.0% ; Score: 2403 ; ID: 4 ; Length: 453
Best local similarity: 100.0% ; Pred. No.: 4 ; ID: 100
Matches: 453 ; Conservative: 0 ; Mismatches: 0 ; Indels: 0 ; Gaps: 0

ALIGNMENTS

Result No.	Score	Query Match	Length	IP	ID	Accession
1	2403	100.0	453	4	Q962X2	Q962X2 homo sapien
2	2360	98.2	415	4	Q962X2	Q962X2 homo sapien
3	2357	98.1	445	4	Q962X1	Q962X1 homo sapien
4	2315	94.2	445	11	Q962X9	Q962X9 ratius norv
5	2182	90.8	415	11	Q962X6	Q962X6 ratius norv
6	2060	85.7	413	11	Q962X7	Q962X7 ratius norv
7	2045	85.1	415	11	Q962X5	Q962X5 cavia porce
8	1975	82.2	497	11	Q962X6	Q962X6 ratius norv
9	1685	70.1	445	11	Q962X9	Q962X9 ratius norv
10	553.5	23.0	528	13	Q962X6	Q962X6 ratius norv
11	511	21.3	440	4	Q962X9	Q962X9 homo sapien
12	511	21.3	440	6	Q962X7	Q962X7 par. A. n. n. l.
13	511	21.3	440	6	Q962X6	Q962X6 quilla qor
14	509	21.2	440	6	Q962X6	Q962X6 poapo pyama
15	506	21.1	399	5	Q962X9	Q962X9 apis mellif
16	492	20.5	462	4	Q962X9	Q962X9 homo sapien
17	489.5	20.4	450	4	Q962X1	Q962X1 homo sapien
18	474.5	19.7	447	4	Q962X0	Q962X0 homo sapien
19	458.5	19.1	477	5	Q962X9	Q962X9 mus muscu

Query Match: 100.0% ; Score: 2403 ; ID: 4 ; Length: 453
Best local similarity: 100.0% ; Pred. No.: 4 ; ID: 100
Matches: 453 ; Conservative: 0 ; Mismatches: 0 ; Indels: 0 ; Gaps: 0


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RESULT 12
Q9N2A7 PRELIMINARY; PRT; 140 AA.
AC Q9N2A7;
DE 01-OCT-2000 (TrEMBLrel. 15, Created)
DI 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DI 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE MUSCARINIC ACETYLCHOLINE RECEPTOR R2 (FRAGMENT).
GN CHR22.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.
OX NCBI_TaxID:9598;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN:CHIMP-2207
KA F. Pan. T. P. Karyakawa II., Saito, N.;
RT "Silver Project."
BL Submitted (25 Feb 2000) to the EMBL, GenBank and DDBJ databases.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G PROTEIN COUPLED RECEPTORS.
DR EMBL: AB041392; BAA94771.1; -.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00247; GPCR_Rhodopsn.
DR PROSITE: PS00247; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS02622; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
FT NON_TER 1
SQ SEQUENCE 140 AA; 49852 MW; 12092346.30371EF CDS;
Query Match 21.3%; Score 511; DB 6; Length 140;
Best Local Similarity 27.7%; Pred. No. 8; Gaps 30;
Matches 122; Conservative 88; Mismatches 165; Indels 66; Gaps 16;
QY 44 LIVATVILGHALVMAVVAAGSTFETPTETLMAATSTVMAVPTVAVVAVVVDGSRVLT 100
DB 7 LSLVILLIILVAVVTPVPSVSEITVWVPTFPAVAVSTVAVTPTPTVAVVAVVAVV 16
QY 134 STVPTVAVVPTVPTVAVVAVVPTVPTVPTVPTVPTVPTVPTVPTVPTVPTVPTVPT 160
DB 67 PVAVSLMLALVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAV 125
QY 164 VLVPTVAVVPTVPTVAVVAVVPTVPTVPTVPTVPTVPTVPTVPTVPTVPTVPTVPT 220
DB 126 FIVAVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVV 181
QY 224 RTQRTFELKLVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAV 276
DB 182 IIVAVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVV 140
QY 277 -----VGLAAVADAGAEATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 335
DB 236 KSPATFATVTEVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVV 301
QY 316 FETVPTVPTVPTVPTVPTVPTVPTVPTVPTVPTVPTVPTVPTVPTVPTVPTVPT 351
DB 235 KLVPTVPTVPTVPTVPTVPTVPTVPTVPTVPTVPTVPTVPTVPTVPTVPTVPT 301
QY 452 KQKVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVV 411
DB 355 RKPVPTFILLALLAVPTVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVV 411
QY 412 YPLCHSPSPRAFTKLL-QPQK 431
DB 414 VALGRATIEPTVPTVPTVPTVPTVPTVPTVPTVPTVPTVPTVPTVPTVPTVPT 421

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RESULT 14
Q9N2A5 PRELIMINARY; PRT; 440 AA.
AC Q9N2A5;
DE 01-OCT-2000 (TrEMBLrel. 15, Created)
DI 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DI 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE MUSCARINIC ACETYLCHOLINE RECEPTOR R2 (FRAGMENT).
GN CHR22.
OS Gorilla gorilla (gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Gorilla.
OX NCBI_TaxID:9594;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN:GORILLA-01;
KA F. Lang. T. Karyakawa II., Saito, N.;
RT "Silver Project."
BL Submitted (25 Feb 2000) to the EMBL, GenBank and DDBJ databases.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G PROTEIN COUPLED RECEPTORS.
DR EMBL: AB041393; BAA94478.1; -.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00247; GPCR_Rhodopsn.
DR PROSITE: PS00247; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS02622; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
FT NON_TER 1
SQ SEQUENCE 440 AA; 48853 MW; 12604240.263764 CDS;
Query Match 21.3%; Score 511; DB 6; Length 440;
Best Local Similarity 27.7%; Pred. No. 8; Gaps 30;
Matches 122; Conservative 88; Mismatches 165; Indels 66; Gaps 10;
QY 44 LIVATVILGHALVMAVVAAGSTFETPTETLMAATSTVMAVPTVAVVAVVVDGSRVLT 100
DB 7 LSLVILLIILVAVVTPVPSVSEITVWVPTFPAVAVSTVAVTPTPTVAVVAVVAVV 66
QY 134 STVPTVAVVPTVPTVAVVAVVPTVPTVPTVPTVPTVPTVPTVPTVPTVPTVPTVPT 160
DB 67 PVAVSLMLALVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAV 125
QY 164 VLVPTVAVVPTVPTVAVVAVVPTVPTVPTVPTVPTVPTVPTVPTVPTVPTVPTVPT 220
DB 126 FIVAVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVV 181
QY 224 RTQRTFELKLVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAV 276
DB 182 IIVAVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVV 140
QY 277 -----VGLAAVADAGAEATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 415
DB 236 KSPATFATVTEVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVV 381
QY 316 FETVPTVPTVPTVPTVPTVPTVPTVPTVPTVPTVPTVPTVPTVPTVPTVPTVPT 351
DB 235 KLVPTVPTVPTVPTVPTVPTVPTVPTVPTVPTVPTVPTVPTVPTVPTVPTVPT 301
QY 452 KQKVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVV 411
DB 355 RKPVPTFILLALLAVPTVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVV 411
QY 412 YPLCHSPSPRAFTKLL-QPQK 431
DB 414 VALGRATIEPTVPTVPTVPTVPTVPTVPTVPTVPTVPTVPTVPTVPTVPTVPT 421

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